

IN THE SPECIFICATION:

Please amend the appropriate paragraphs of specification in accordance with proposed changes as outlined hereinbelow:

Please amend page 7, first full paragraph, as follows:

According to the present invention, when the term group used as the term has hierarchy like gene ontology ([refer to www.geneontology.org](http://www.geneontology.org)) and a family name, drawing the network in an upper hierarchy allows to show the network concisely, to show considering the relationship between terms with a low expression frequency and statistical uncertainty, or to show the network with the node (term) connecting conditions eased.

Please amend the paragraph that bridges page 12-13, as follows:

The data storage system 4 of Fig. 1 previously accumulates function information such as interactions, genes and proteins previously extracted manually or automatically extracted using a sentence pattern from texts as the binary relations (42, 43 of Fig. 1) and the interaction information and configuration function information (44) taken from other databases. To use the co-occurrence information on terms in the texts, the terms, the text including the terms and the positions of terms in the text are accumulated as a table (41). When terms to be the object are few, co-occurrence of all term pairs may be previously calculated as a weight of the binary relation and given in the table. A flow to automatically extract such information is shown in Fig. 3. The object data includes various kinds of science-specialized magazines, and magazines registered in NCBI ([refer to www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)) PUBMED-abstract, PUBMED-central and the like. Object theses are desirably narrowed to only an abstract/thesis of living species to be the object using a mesh term when the PUBMED is used because information on other living species is not mixed. Connection to the data storage system may be made through the Internet.

Please amend the paragraph that bridges page 23, line 24 to page 25, line 1, as follows:

An example of the term network when data on appearance of a DNA-array is used is shown in Fig. 13. It corresponds to step 9 of Fig. 2. In Fig. 13, an upper section 71 shows a portion linking a gene group used in clustering corresponding to the query 1 and the query 2 by a network of terms. A lower section 72 shows an example of clustering according to the experimental results in which a hierarchical clustering based on expression data of DNA array is shown. The query 1 includes all terms classified into the biological process of gene ontology, and the query 2 describes the network of terms when the gene names clustered are included into the same group by the expression data. In this example, the terms of the query 1 not showing a significant network are not

shown (an upper section 71). A hierarchical structure of query 1 terms on the dictionary side of a cell cycle, a DNA replication and a mitotic cell cycle is shown in an upper section 73. According to the experimental data, STE7 belonging to cluster A is different from genes belonging to another A, does not have a network significant with the terms relevant to the cell cycle but has a network with a response to pheromone. Therefore, it is ~~miss~~ mis-clustering caused by the experiment noise, and it is suggested that it originally belongs to cluster B. It is preferable that the network and genes that become candidates for the ~~miss~~ mis-clustering are highlighted because the array data covers a lot of genes. On the other hand, it is suggested that YDR324 is possibly a new gene not having a network with a response to pheromone but related to the response to pheromone without having a significant network with other terms.